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Electronic Length Frequency Analysis. A Revised and Expanded User's Guide to ELEFAN 0, 1 and 2 (2nd Edition)

by

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Abstract

This guide presents an updated and extended version of the ELEFAN 0, ELEFAN 1 and ELEFAN 2 programs for Electronic LEngth Frequency ANalysis. These programs can be used to estimate the parameters of a (seasonally oscillating) growth equation, total mortality (Z = P/B ratio) and related parameters, as well as to derive seasonal patterns of recruitment. Input data are length-frequency samples collected at regular or irregular intervals, and optionally, growth information obtained from tagging-recapture experiments or from ageing studies. The revised programs incorporate modifications suggested by recent simulation studies aimed at identifying sources of bias in the original ELEFAN procedures. The programs are available in three different versions for :

		Memory requirement
(i)	Radio Shack TRS 80 Models I/III (three or one 5 1/4' diskette(s) in TRS BASIC II for Model I or III, respectively)	38K
(ii)	Apple II (CP/M) and compatibles (one double-sided 5 1/4' diskette, one side in Microsoft BASIC, the other in compiled MBASIC) and	40K
(iii)	IBM PC and compatibles (one 5 1/4' diskette with compiled and uncompiled BASICA programs).	102K

This guide describes the operation of versions (i) to (iii). A test data set, referring to the bivalve *Syndosmya alba* and printout of actual runs are provided. Readers are invited to contact any of the authors regarding any problem that might arise when using this ELEFAN package.

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List of Exhibits

Introduction

This user's guide to the ELEFAN 0, 1 and 2 programs (henceforth called "guide"), presents a revised and expanded version of a set of computer-based methods for the estimation of growth, mortality and related parameters of fish and vertebrate populations, and known as Electronic LEngth Frequency ANalysis (ELEFAN). The methods, initially presented in Pauly and David (1980, 1981) and Pauly (1982) have found wide application throughout the world (see below and References section).

In February 1985, a conference on the "Theory and Application of Length-Based Methods in Stock Assessment" was held in Mazarra del Vallo, Sicily, Italy, at which the ELEFAN programs and a number of other length-based methods were reviewed (Pauly 1985d, Pauly and Morgan 1985; Morgan and Pauly 1987). At this conference, simulation studies by Hampton and Majkowski (1987) and Rosenberg and Beddington (1987) were presented, in which the performance of the ELEFAN 1 and 2 programs was assessed, based on simulated length-frequency data sets generated with known values of growth and mortality parameters.

The version of the ELEFAN 1 and 2 programs presented here incorporates the results of these analyses, and thus represent a "second generation" of ELEFAN programs (another second generation version of ELEFAN 0, 1 and 2, for use with Hewlett-Packard computers, is also available, see Saeger and Gayanilo 1985). The new versions presented here include novel approaches for growth parameter estimation also presented at this conference, notably a method, modified from Morgan (1987) for the *simultaneous* analysis of length-frequency and tagging/recapture and/or length-age data, and a method for direct estimation of L_∞ and Z/K from length-frequency data (Wetherall 1986, Pauly 1986, Wetherall et al. 1987).

Important modifications of the ELEFAN 0 program over the original version (David et al. 1982) are:

a) Improved entry and editing routines, and
b) Provision for the entry of probabilities of capture, by length and correction of a length-frequency data set for selection effects (i.e., creation of a new, corrected data set).

Important modifications of the ELEFAN 1 program over the original version (Pauly et al. 1980) are:

c) Supression of "drifting" as described in Pauly et al. (1980), i.e., of the output of impossibly low values of K and associated values of ESP/ASP>1 (see Pauly 1985b and section 2.4).
d) Redefinition of "scores" associated with the largest fish and/or with isolated peaks, such as to counteract (1) the tendency of ELEFAN 1 to overestimate L_∞ and (2) for single, isolated peaks based on a few animals to strongly affect growth parameter estimation.
e) Output of a table of ESP/ASP values to help assess quality of growth parameter estimates associated with highest ESP/ASP values (as used in very early versions of ELEFAN 1, and in Brouard and Grandperrin 1984).
f) Incorporation of a routine which allows simultaneous analysis of length-frequency data and tagging/recapture and/or length-at-age data, based on an approach from Morgan (1987).

Important modifications of the ELEFAN 2 program are:

g) Addition of new weighting modes for combining a series of length-frequency samples into one single total sample representative of the steady-state population.
h) Inclusion of a new method for estimation of L_∞ and Z/K from length-frequency data as developed, using a rigorous theoretical approach by Wetherall et al. (1987).

This latter routine, which can be implemented immediately after the ELEFAN 0 program has the advantage of providing an estimate of L_∞, it considerably cuts computation time while providing

a well-defined estimate of a parameter which ELEFAN 1 often has problems estimating reliably (Rosenberg and Beddington 1987).

Unfortunately, there will be instances when this routine will not work; in such cases, ELEFAN 1 will have to be used with variable L_∞ (The user is advised, however, not to let L_∞ wander too far from the size of the largest fish, as ELEFAN 1 if anything, tends to overestimate L_∞).

Modification (g) was added to allow the use of ELEFAN 2 in temperate areas, where strong seasonal growth oscillations can distort markedly the size-frequency distribution of total samples accumulated over longer periods (T. Brey, pers. obs.; H. Salzwedel, pers. comm.).

Modification (f) anticipates a program implemented for use with IBM PC microcomputers, and which will be included as ELEFAN 5 in a comprehensive guide to the ELEFAN system (also including ELEFAN 0, 1, 2, 3, 4), to be published soon (see Morgan and Pauly 1987). Users of this specific routine should, in the meantime, credit Morgan (1987) for the idea of combining the ELEFAN 1 approach with tagging/recapture and/or length-at-age data.

Modification (e) provides an output, i.e., a response surface (see Table 10 as example) which can be used for a subjective assessment of the reliability of estimates of growth parameters obtained by ELEFAN 1. One aspect of the modifications in (d) are analogous to modification (c) in that the same points (here: negative points associated with large fish) are prevented from being counted over and over again when the ESP value is computed (see section 2.3). The other aspects of this modification is that isolated peaks, i.e., peaks "surrounded by zero frequencies and which are previously multiplied by a factor whose value descended *arithmetically* with ascending number of surrounding zero frequencies (i.e., from 1.0 to 0.2, in steps of 0.2, for 0 to 4 zeros) are now multiplied with factors whose value descends *geometrically* with ascending number of surrounding zeros (see Table 2, section 2.3).

Modification (b), used in the proper fashion, should also contribute to improved growth parameter estimates. What is meant here is that the ELEFAN 1 and 2 programs can be used iteratively as follows:

(i) First, estimate L_∞ using ELEFAN 2B;
(ii) Estimate the other growth parameters in a first pass with ELEFAN 1;
(iii) Construct a catch curve and associated probabilities of capture for small animals using ELEFAN 2A;
(iv) Use the estimated probabilities of capture to correct the original length-frequency data for selection effects (using ELEFAN 0);
(v) Reestimate growth parameter (other than L_∞) in a second pass with ELEFAN I;
(vi) Reestimate catch curve and derived quantities using ELEFAN 2A with the new growth parameter and the original length-frequency data file, etc. (see Fig. 1).

Usually, one single iteration will suffice to bring convergence about, i.e., to obtain growth parameters not biased by selection effects (such parameters will usually include a higher value of K!). However, if very low probabilities of capture (say <0.01) are used to correct the length-frequency data, this iterative procedure will not work because very low probabilities would overcompensate for the effects of selection.

Modification (a) is straightforward enough, and comments on it are not really needed. Rather we shall reiterate here the need, when working with the ELEFAN programs, to use length-frequency data as representative as possible of the population sampled, covering a range of length as wide as possible, and biased as little as possible by size-selective sampling gears and uneven distribution of the sampled population. Also, care should be taken to use samples obtained at intervals as regular

as possible (this is however *not* a necessary requirement), and of sizes not varying too widely (see Pauly 1984d for a step-by-step approach to obtain representative length-frequency samples from stratified random trawl surveys).

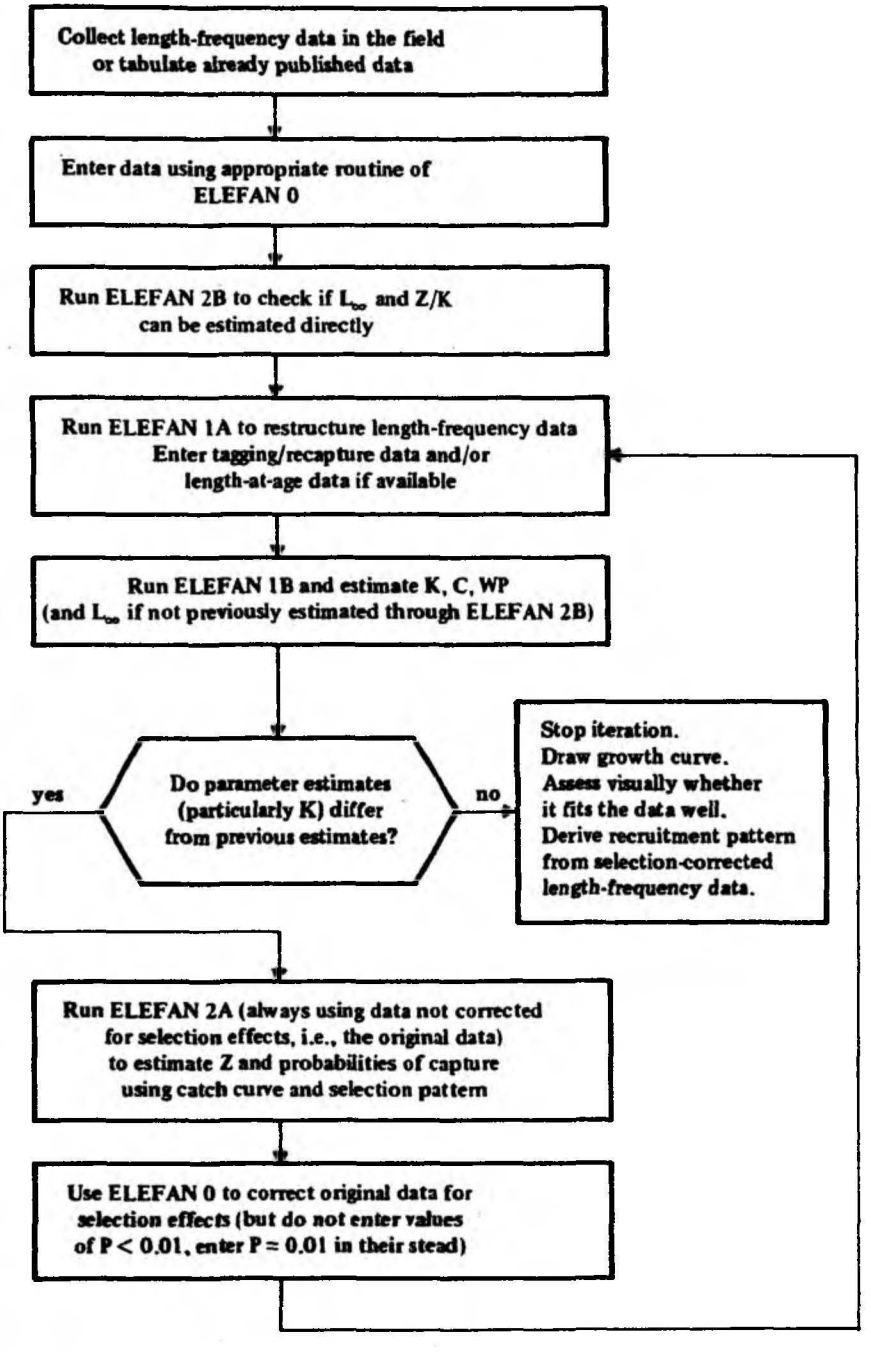


Fig. 1. Flow chart showing the links between the ELEFAN programs.

A modification which affects both ELEFAN 1 and 2 is that the growth equation used (see section 2.4) assumes the parameter D in the generalized von Bertalanffy equation (see Pauly and David 1981 and Pauly 1984c) to be equal to 1 (i.e., the parameter does not occur). This has the important implications that:

(i) computation time is reduced for ELEFAN 1, and

(ii) users of the programs are not burdened with what probably was a superfluous refinement.

We hope that this new version of the ELEFAN 0, 1 and 2 programs will contribute toward the ELEFAN approach fulfilling its promise of simple, cheap and reliable fish stock assessments (Morgan 1983; Mathews 1987), as well as help benthologists and others working on growth and production of invertebrates. Toward this aim, we have added to the reference list - over and beyond the items cited in the text - a number of references presenting applications of the ELEFAN programs to fish and invertebrate stocks throughout the world. Users of this guide are invited to familiarize themselves with these papers, because it is such familiarity which will allow them to make the best use of their data and of the programs presented here.

Good luck!

2. User's guide, by program

The structure of the ELEFAN program package and the links between the different programs are demonstrated by the flow chart in Fig. 1.

This ELEFAN package consists of the following programs:

START	:	Main menu program
ELEFAN 0	:	Data file management
ELEFAN 1A	:	Restructuring of length-frequency data; Optional input of tagging data and/or length-at-age data
ELEFAN 1B	:	Identification of the best fitting growth curve
ELEFAN 2B	:	Estimation of total mortality; Derivation of seasonal patterns of recruitment
ELEFAN 2B	:	Estimation of L_∞ and Z/K from mean lengths

The package is available[a] in three different versions:

(i) Radio Shack TRS 80 Models I/III with at least 38K of RAM and two 5 1/4' disk drives

(ii) Apple II (+,e or c) with CP/M card (or compatibles), 40K of RAM and either two 5 1/4' disk drives or 3 1/2' Unidisk[b].

(iii) IBM PC and compatibles with at least one 5 1/4' disk drives and at least 102K of RAM.

The output routines assume that an EPSON printer (or compatible) is connected.

2.1 START: Main menu program

Every ELEFAN program (0, 1A, 1B, 2A, 2B) has to be accessed by the program START. Finishing the work with any ELEFAN program will automatically lead back to the main menu shown below.

---

[a] From the Director, Resource Assessment and Management Program, International Center for Living Aquatic Resources Management (ICLARM), MC PO Box 1501, Makati Metro Manila, Philippines, for US$15.00 payable with cheque drawn to a US-based bank, or with UNESCO coupons, available from UN outlets. Please specify exactly which version you want.

[b] a separate diskette with a program generating HIRES graphics for this version of the ELEFAN package, as described by Liew (1986) is available separately from ICLARM, under the conditions in (a).

```
                    ELEFAN
        ELECTRONIC LENGTH FREQUENCY ANALYSIS
                MS/DOS - VERSION
        (c) 1985 DANIEL PAULY AND THOMAS BREY
                (Update of January 1988)
        BY D. PAULY, M. SORIANO AND J. M. VAKILY

                MAIN MENU FOR ELEFAN PROGRAMS

ELEFAN 0     :  FILE MANAGEMENT                          <1>

ELEFAN 1A    :  DATA RESTRUCTURING
                INPUT OF AGE-LENGTH DATA                 <2>

ELEFAN 1B    :  GROWTH CURVE PARAMETERS                  <3>

ELEFAN 2A    :  CATCH CURVE + RECRUITMENT PATTERN        <4>

ELEFAN 2B    :  ESTIMATION OF L∞ AND Z/K                 <5>

END                                                      <6>

                                    SELECT NUMBER :
```

2.2 ELEFAN 0: Data file management

ELEFAN 0 is a program for length-frequency data handling and files management. Its various routines are discussed in the actual run of this program. The limitations on the structure and size of length-frequency data files are displayed upon accessing the program.

```
        PROGRAM ELEFAN 0
    DATA INPUT AND FILE MANAGEMENT PROGRAM

          *** LIMITATIONS AND WARNINGS ***

    THIS PROGRAM CAN HANDLE FILES CONSISTING OF UP TO
            24 SAMPLES and
            30 MIDLENGTHS (= CLASSES)

    IMPORTANT!
    When entering LENGTH-FREQUENCY DATA, frequencies
    must be entered as INTEGER VALUES.
    (Largest acceptable frequency number is 32767)
```

Length-frequency data of *Syndosmya alba* from Kiel Bay will be used for illustration throughout this guide. Table 1 shows a printout of the data. Note that MIDL. stands for "midlength" or midpoint of a length class.

Table 1. Printout of *Syndosmya alba* data (ELEFAN 0).

B:SYSF11.DAT
Syndosmya alba / SF 04.1976 — 06.1977 / 1 mm classes

Sample No.		1	2	3	4	5	6	7
Day.Month		17.04	2.07	19.09	15.12	18.02	20.04	24.06
Class	Midlength							
1	1.5	0	0	0	2	0	2	0
2	2.5	0	1	9	1	1	1	0
3	3.5	0	1	34	3	0	1	0
4	4.5	1	0	96	3	0	1	0
5	5.5	1	1	68	4	2	1	0
6	6.5	1	0	50	21	4	6	0
7	7.5	3	0	16	33	9	7	1
8	8.5	9	3	2	47	26	12	5
9	9.5	5	3	1	34	30	14	10
10	10.5	0	6	1	16	14	3	3
11	11.5	3	1	0	9	11	0	0
12	12.5	1	0	0	4	4	0	0
13	13.5	1	0	0	3	2	2	0
14	14.5	0	1	0	2	2	1	0

Actual run of ELEFAN 0

The submenu for this routine contains 8 options shown and described below:

```
*** ELEFAN 0 MAIN MENU ***

CREATE NEW FILE:                                          <1>
SELECT SAMPLES FROM OLD FILE:                             <2>
EDIT OLD FILE:                                            <3>
EDIT OLD FILE: CORRECTION FOR SELECTION EFFECTS:          <4>
EDIT OLD FILE: CHANGE LENGTH CLASS SIZE:                  <5>
DATA FILE LIBRARY MANAGEMENT:                             <6>
OUTPUT A FILE ON PRINTER:                                 <7>
BACK TO ELEFAN MAIN MENU:                                 <8>
                                        SELECT NUMBER:
```

<1> CREATE NEW FILE

To create a new length-frequency file, follow the flow of input requirements as given below:

i) Inputs for data file specifications:
- DATA FILE NAME
- ADDITIONAL INFORMATION
- NUMBER OF SAMPLES (max. = 24)
- LOWEST MIDLENGTH (lowest = 0.25)
- HIGHEST MIDLENGTH
- INTERVAL SIZE

ii) Inputs for each sample:

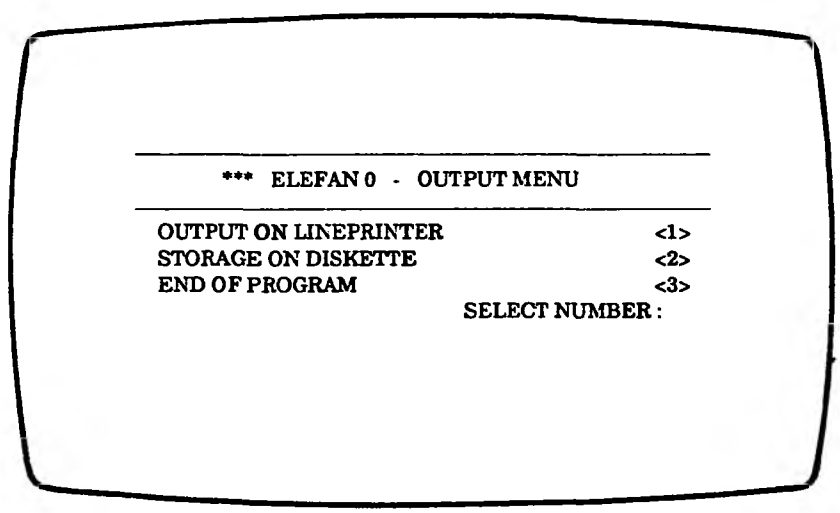
- MONTH (of sampling)
- DAY (of sampling)
- LOWEST MIDLENGTH (of the sample)
- HIGHEST MIDLENGTH (of the sample)

Note: If the sampling day is unknown, use day = 15; if samples have been pooled, use "average" sampling date

iii) Input frequency per length class

After the last sample has been entered, the file is displayed through the REVIEW FOR ERRORS routine. Here, incorrect sampling dates or frequency values can be corrected.

When the REVIEW routine has been completed, the program proceeds to OUTPUT MENU for disk saving or printing of data:



<2> SELECT SAMPLES FROM OLD FILE

This option will create a new file from an existing data file. The program asks for the name of the old data file and loads it in memory. The dates of all samples and frequencies are then displayed on screen and the user is asked to select samples to be included in the new file.

<3> EDIT OLD FILE

Existing data files may be edited by selecting this option. The REVIEW FOR ERROR routine is linked after loading the filename to edit. Erroneous entries can then be corrected. The corrected file may be stored under a new name or under the old name (the latter will overwrite the old file).

<4> EDIT OLD FILE: CORRECTION FOR SELECTION (probabilities of capture)

Probabilities of capture are estimated by means of a catch curve (i.e., program ELEFAN 2A) or through a gear selection experiment (not discussed here, but see Pope et al. 1975). After loading the data file, the program asks for the probabilities of capture (p), beginning with the lowest length class ($F_i = F_i/p_i$). Probabilities of capture < 0.0001 should be set equal to 0.0001 to prevent inflation of corrected frequencies. Otherwise the maximum corrected frequency is set to 32767.

<5> EDIT OLD FILE: INCREASE LENGTH CLASS SIZE

This option allows for the regrouping of frequencies to larger classes (this is obtained by multiplying the original class interval by a factor of 2, 3 or 4), e.g., from 1 mm length classes to 2 mm length classes.

<6> DATA FILE LIBRARY MANAGEMENT

This option allows for the deletion of files from the disk.

<7> OUTPUT A FILE ON PRINTER

This option allows for data files to be printed out using an EPSON or compatible printers.

<8> BACK TO ELEFAN MAIN MENU

This will chain back to program START.

2.3 ELEFAN 1A: Restructuring of length-frequency data and optional input of tagging and/or length-at-age data

ELEFAN 1A provides a link between ELEFAN 0 and ELEFAN 1B by restructuring a length frequency data file created through ELEFAN 0 for use in growth parameter estimation through ELEFAN 1B. ELEFAN 1A also allows for entry of tagging/recapture and/or length-at-age data.

Restructuring of length-frequency data

The aim in restructuring a set of length-frequency samples is to arrive at an objective identification (or definition) of the peaks corresponding to "cohorts", independently of the height of the peaks themselves and of any assumed form for the peaks (i.e., no assumptions are made about the shape of the length-frequency distribution within a single cohort).

For a given sample of length-frequency data (F_i, i = 1 to n, n = no. of classes), the following steps describe the procedure for restructuring length frequency data (each step is demonstrated in Table 4 using sample No. 6 of *Syndosmya alba* data):

(a) For each length class i of sample k compute the moving average over 5 length classes (MA_i).

$$MA_i = \sum_{j=i-2}^{j=i+2} F_j/5 \qquad \text{where } F = 0 \text{ for } i = -1, 0, n+1, n+2$$

(b) Compute adjusted frequency (AF_i).

$$AF_i = F_i/MA_i$$

(c) Compute relative adjusted frequency (F'_i) and subtract 1 to identify the peaks ($F'_i > 0$) and troughs ($F'_i < 0$).

$$F'_i = (AF_i/\overline{AF}) - 1$$

At this stage the length-frequency sample consists of:

i) peaks ($F'_i > 0$)
ii) troughs ($-1 \leq F'_i < 0$)
iii) points which are neither peaks nor troughs ($F'_i = 0$)
iv) points which correspond to the original zero values ($F'_i = -1$).

The procedure described in (1) - (3) has the disadvantage that the height of positive values will be inflated by adjacent zero frequencies, if any such value "surround" the length classes in question. If a frequency value F is surrounded by two zero frequencies on each side, the moving average MA will be equal to $F_i/5$ and $FA_i = F_i/(F_i/5) = 5$.

Considering that the "points" of peaks surrounded by nonzero frequencies are generally in the range of 1 or less, all positive values F' referring to frequencies surrounded by zero frequencies are multiplied by a factor of $1/(2^{nz})$ for nz surrounding zero frequencies (see Table 2).

Table 2. Adjustment of peaks F_i for adjacent zero frequencies (i.e., for frequencies one or two classes to the left or right of a given length class).

No. of zero frequencies included in computation of MA_i	Adjustment of F'_i
1	$F'_i = 0.5000 * F'_i$
2	$F'_i = 0.2500 * F'_i$
3	$F'_i = 0.1250 * F'_i$
4	$F'_i = 0.0625 * F'_i$

(d) An additional, optional procedure to reduce the influence of low frequency values is implemented in the version of ELEFAN described here. All positive restructured values F'_i are divided by a factor whose value depends on F_i.

$$F'_i = F'_i/SQR(1+2/F_i)$$

This procedure will be useful if length-frequency data including a lot of low values ($F_1 < 10$) are examined. The effect of this procedure (not included in previous versions of ELEFAN) is shown in Table 3.

Table 3. Adjustment of peaks for low frequency values.

Frequency value (F)	Adjustment of F'
1	$F'_i = F'_i/1.732$
2	$F'_i = F'_i/1.225$
3	$F'_i = F'_i/1.106$
4	$F'_i = F'_i/1.061$
5	$F'_i = F'_i/1.039$
10	$F'_i = F'_i/1.010$

(e) All values = -1 are set back to zero, the sum of all positive values SUM(+) and the sum of all negative values SUM(-) is calculated and all negative values are multiplied by the ratio SUM(+)/SUM(-). This results in a restructured length-frequency sample with equal sums of positive and negative values.

(f) The final step is to replace all negative values occurring in the highest length class of a length-frequency data set by zero values and to divide all negative values occurring in the penultimate length class by 2. Simulation studies with the ELEFAN method showed that this contribute to reducing overestimate of L_∞ (see Introduction).

Table 4. Illustration of restructing procedure using sample No. 6 of *Sydosmya alba* data.

Mid-length	F_i	MA_i	AF_i	$AF_i/\overline{AF}$	Subtract 1	Adjust for zero freq.	Adjust for F_i	Neutralized
1.5	2	0.8	2.500	2.187	+1.187	0.297	0.242	0.242
2.5	1	1.0	1.000	0.875	-0.125	-0.125	-0.125	-0.054
3.5	1	1.2	0.833	0.729	-0.271	-0.271	-0.271	-0.117
4.5	1	1.8	0.556	0.486	-0.514	-0.514	-0.514	-0.222
5.5	1	3.0	0.333	0.291	-0.709	-0.709	-0.709	-0.307
6.5	5	5.2	0.962	0.842	-0.158	-0.158	-0.158	-0.069
7.5	7	7.8	0.897	0.785	-0.215	-0.215	-0.215	-0.093
8.5	12	8.2	1.463	1.280	0.280	0.280	0.280	0.280
9.5	14	7.2	1.944	1.701	0.701	0.351	0.349	0.349
10.5	3	5.8	0.517	0.452	-0.548	-0.548	-0.548	-0.463
11.5	0	3.8	0	0	-1	-1	-1	-0
12.5	0	1.2	0	0	-1	-1	-1	-0
13.5	2	0.6	3.333	2.916	1.916	0.240	0.196	0.196
14.5	1	0.6	1.667	1.458	0.458	0.057	0.033	0.033
	$\overline{AF}$ = 1.143					SUM(+) = 1.098		
						SUM(-) = 2.540		
						ratio of SUM(+)/SUM(-) = 0.432		

Conversion of length-at-age data into growth increment data

Because of mathematical problems related to estimation of t_0 and the inclusion of length-at-age data in the ELEFAN procedure, length-at-age data are here converted into growth increment data. The growth increment data, having a structure resembling tagging/recapture data, are analyzed as if they were, in fact, tagging/recapture data (or tagging data for short). A maximum number of 10 ages can be entered. Since seasonal oscillations of growth are considered by the model incorporated in ELEFAN 1B, it is important to know the date of sampling of the length-at-age data. Ages are entered in the form of sampling date and number of years completed until sampling took place. For each age, 10 lengths can be entered.

The program then sorts the ages in ascending order (age_1, age_2,... age_{10}). With a maximum of 10 ages, 10-1 (=9) age pairs (e.g., age_i and age_2, age_2 and age_3 ....age_9 and age_{10}) are identified. For 10 lengths per age, 10 * 10 combinations of growth increments are then derived for each age pair (length at age_1 to length at age_{i+1}). Thus, the maximum number of growth increments for 10 ages with 10 lengths each is 9 * 10 * 10 (=900).

A maximum number of 100 pairs of age_i/length, and age_{i+1}/length is then selected by picking out growth increments closest to the mean growth increments of each age interval, then gradually moving toward extreme values (high and low). In order to get a more or less equal distribution of data pairs over the whole available length range, this range is divided into 10 intervals of equal size. Each selected growth increment is sorted into one of these 10 length intervals with respect to its value of $(L_i + L_{i+1})/2$. A maximum number of 10 growth increments/length-interval is possible, which corresponds to the overall maximum number of 100 combinations. Table 5 shows a set of length-at-age data derived from an assumed growth curve for *Syndosmya alba*, based on the length-frequency data in Table 1 (note that, usually, length-at-age data are obtained by counting annuli or daily rings on hard parts).

Table 5. Length-at-age data of *Syndosmya alba*.

date of sampling (day/month)	number of years completed	length (mm)
15/12	0	8.0, 8.5, 8.5, 9.0
30/04	0	8.5, 9.0, 9.0, 9.5
02/07	0	9.5, 10.0, 10.5
30/04	1	13.0, 13.5, 13.5
30/04	2	14.5, 14.5

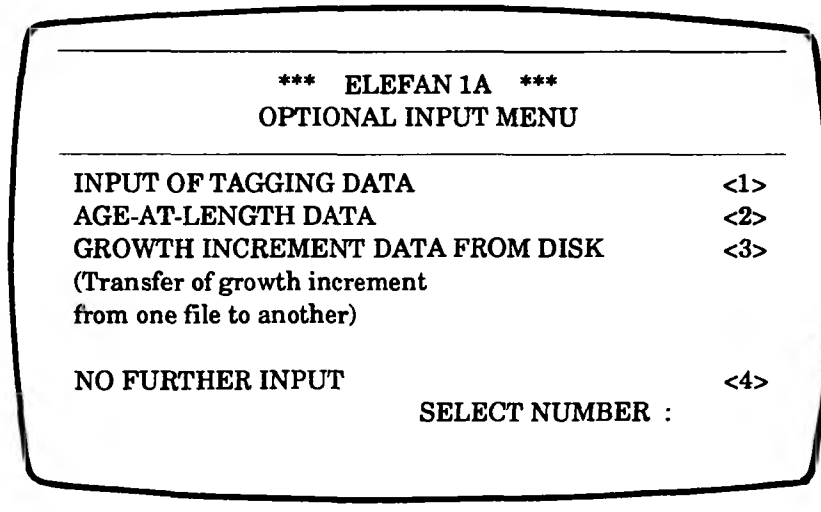
Actual run of ELEFAN 1A

The program is accessed via the main menu START, and can only use data created and stored using ELEFAN 0. After loading the data file, the program asks:

ADJUSTMENT OF PEAKS: (see Table 3 of manual)
OPTIONS ARE <A> AND <B> (default is <A>)?

If A is entered, only the adjustment for surrounding zero frequencies is performed. If B is selected the restructuring will also account for low sample sizes. Then the program proceeds to the restructing of length frequency data. The restructured data are then displayed on screen together with the Sum of Peaks (ASP).

After restructuring of the length-frequency file, the optional input menu appears on screen to allow entry for tagging data and/or length-at-age data or to retrieve growth increment data from the disk file.



<1> INPUT OF TAGGING DATA

This option allows entry of up to 100 pairs of tagging/recapture data. The input procedure is shown as follows:

ENTER NUMBER OF DATA PAIRS (<=100):
DATA PAIR No *x*

TAGGING - DAY (1-31):
MONTH (1-12):
YEAR (last 2 digits):
LENGTH:
IS THIS CORRECT? (Y/N)

RECAPTURE - DAY (1-31)
MONTH (1-12):
YEAR (Last 2 digits):
LENGTH:
IS THIS CORRECT? (Y/N)

After all data are entered, they are displayed to allow the user to check and correct the entries.

<2> INPUT OF LENGTH-AT-AGE DATA

The maximum size of the data matrix is 10 age * 10 lengths-at-age. The age data must be entered in ascending order of ages.

Data input procedure (*x*th age, first length)

x th AGE:

DAY (1-31): ENTER 999 WHEN DONE
MONTH (1-12):
NUMBER OF YEARS COMPLETED UNTIL SAMPLING
IS THIS CORRECT? (Y/N):

The length data for each age are reviewed before proceeding to entry of next age. The computer then follows the procedure for selecting up to 100 growth increments described above. The selected growth increments and their distribution over the available length range are displayed.

<3> GROWTH INCREMENT DATA FROM DISK

If tagging data or length-at-age data have been stored on disk during a previous run of ELEFAN 1A, they can be retrieved. It is not possible to use this option together with option 1 or option 2!

ENTER FILENAME:
IS THIS CORRECT ? (Y/N)

If the data file selected does not contain growth increment data the program goes back to the OPTIONAL INPUT MENU.

<4> NO FURTHER INPUT

When the new restructured data file is ready for disk saving or printing, this option will take the user to the very last procedure included in ELEFAN 1A, the OUTPUT ROUTINE (this routine has the same menu as described in the previous section). If the data file is printed out on lineprinter, any growth increment data will optionally be printed. Table 6 shows the restructured length-frequency data of *Syndosmya alba* and Table 7 shows the growth increments selected from the length-at-age data in Table 5.

Table 6. Printout of restructured length-frequencies of *Syndosmya alba* (ELEFAN 1A).

B:SYSF11.DAT
Syndosmya alba / SF 04.1976 — 06.1977 / 1 mm classes
RESTRUCTURED LENGTH-FREQUENCY DATA / OPTION A

Sample No.		1	2	3	4	5	6	7
Day.Month		17.04	2.07	19.09	15.12	18.02	30.04	24.06
Class	Midlength							
1	1.5	0.000	0.000	0.000	0.197	0.000	0.297	0.000
2	2.5	0.000	0.116	-0.528	-0.286	0.225	-0.060	0.000
3	3.5	0.000	0.071	-0.024	0.239	0.000	-0.131	0.000
4	4.5	0.133	0.000	1.210	-0.352	0.000	-0.248	0.000
5	5.5	-0.186	0.116	0.524	-0.470	-0.176	-0.341	0.000
6	6.5	-0.534	0.000	0.275	0.044	-0.250	-0.077	0.000
7	7.5	-0.211	0.000	-0.264	0.275	-0.189	-0.104	-0.377
8	8.5	0.650	-0.042	-0.711	0.671	0.441	0.280	0.017
9	9.5	0.076	-0.127	-0.602	0.313	0.534	0.350	0.533
10	10.5	0.000	0.389	0.120	-0.155	-0.110	-0.264	-0.173
11	11.5	0.190	-0.700	0.000	-0.190	-0.077	0.000	0.000
12	12.5	-0.062	0.000	0.000	-0.261	-0.201	0.000	0.000
13	13.5	-0.031	0.000	0.000	-0.037	-0.117	0.239	0.000
14	14.5	0.000	0.178	0.000	0.048	0.038	0.057	0.000

ASP = 6.472999.

Table 7. Growth increments derived from length-at-age data of *Syndosmya alba* (ELEFAN 1A).

B:SYSF11.DAT
SELECTED GROWTH INCREMENTS

The 35 growth increments below were selected by ELEFAN 1A from 43 increments generated from the age length data entered previously. The selection process differs from that used in Brey and Pauly (1986, p. 14); it is now wholly deterministic and starts by picking those growth increments that are closest to the mean growth increments of each age interval, then gradually moves toward extreme low and high values.

No.	L(1)	t(1)	L(2)	t(2)
1	8	.96	9	1.33
2	8	.96	9	1.33
3	8	.96	9.5	1.33
4	8.5	.96	8.5	1.33
5	8.5	.96	8.5	1.33
6	8.5	.96	9	1.33
7	8.5	.96	9	1.3
8	8.5	.96	9	1.33
9	8.5	.96	9	1.33
10	8.5	.96	9.5	1.33
11	8.5	.96	9.5	1.33
12	8.5	1.33	10	1.5
13	9	.96	8.5	1.33
14	9	1.33	9.5	1.5
15	9	1.33	9.5	1.5
16	9	1.33	10	1.5
17	9	1.33	10	1.5
18	9	1.33	10.5	1.5
19	9	1.33	10.5	1.5
20	9.5	1.33	9.5	1.5
21	9.5	1.5	13	2.33
22	9.5	1.5	13.5	2.33
23	9.5	1.5	13.5	2.33
24	10	1.5	13	2.33
25	10	1.5	13.5	2.33
26	10	1.5	13.5	2.33
27	10.5	1.5	13	2.33
28	10.5	1.5	13.5	2.33
29	10.5	1.5	13.5	2.33
30	13	2.33	14.5	3.33
31	13	2.33	14.5	3.33
32	13.5	2.33	14.5	3.33
33	13.5	2.33	14.5	3.33
34	13.5	2.33	14.5	3.33
35	13.5	2.33	14.5	3.33

2.4 ELEFAN 1B: Identification of the best fitting growth curve

This program fits a von Bertalanffy growth curve to a given set of restructured length-frequency samples or to a set of restructured length-frequency samples combined with tagging data and/or length-at-age data (expressed as growth increments, as described in the previous section).

Available Sum of Peaks (ASP) and Explained Sum of Peaks (ESP)

Let us assume a set of ns restructured length-frequency samples. Usually we will find a number of np peaks (= runs of positive values) within each of the ns samples. If it is assumed that each peak corresponds to a distinct age class, it follows that any growth curve going through a certain peak will be able to "hit" only one of the length classes constituting this peak. Thus, by definition, the maximum sum of positive point values that can be accumulated by a growth curve fitted to a set of

ns samples equals the sum of the highest values of all np peaks in all ns samples. This sum is called Available Sum of Peaks (ASP), and

$$ASP = \sum_{k=1}^{ns} \sum_{i=1}^{np} \text{highest value of peak (k, i)}$$

Any growth curve passing through a restructured length-frequency data matrix will "hit" a number of points (= length L at time t) within this matrix. Adding up the restructured frequency values corresponding to these points, a sum will be obtained which can never exceed the ASP*. A curve which goes through many peaks while avoiding most of the troughs will accumulate a high sum of points. This curve will interconnect a large number of peaks and is considered here to explain the positions of these peaks as the result of individual growth of the animals investigated. Therefore the sum of values corresponding to the points "hit" by the curve is called Explained Sum of Peaks (ESP). The ratio ESP/ASP is the index for the goodness of fit of a growth curve. With regard to the definition of ASP and ESP the ESP/ASP-ratio can never exceed 1, and may be viewed as roughly corresponding to the parameter r^2 in correlation analysis (if one neglects the fact that ESP/ASP may reach values $<<0$ for particular "bad" combinations of growth parameters).

Index of goodness of fit for tagging data and length-at-age data

The calculation of the index of goodness of fit is the same for tagging data and converted length-at-age data (i.e., growth increment data). Therefore reference will be made in the following to tagging data only.

A set of tagging data consists of a number nt of data pairs L_1, t_1 and L_2, t_2 which are one length at time t_1 and a second length at time t_2. The change in length per time (i.e., the growth rate) is given by

$$\Delta L/\Delta t = (L_2-L_1)/(t_2-t_1)$$

With any set of growth parameter values K, L_∞, C, and WP one can also calculate a theoretical length increment by asking: what length would an animal of length L_1 at time t_1 have at time t_2 if its growth follows exactly the growth equation implied by the current set of growth parameter values?

For each of the tagging data pairs, the following calculations are performed:

i) Calculation of the empirical length increment $\Delta L/\Delta t$
ii) Calculation of an internal "t_0" using the current growth parameter values and L_1, t_1
iii) Calculation of the expected length L'_2 at time t_2 using the growth parameter values and the "t_0" value.
iv) Calculation of the theoretical length increment $\Delta L'/\Delta t$
v) Calculation of the difference between empirical and theoretical length increments
$d(incr) = \Delta L/\Delta t - \Delta L'/\Delta t$

The variance v_e of the empirical length increment data is:

$$v_e = (\Sigma(\Delta L/\Delta t)^2 - (\Sigma\Delta L/\Delta t)^2/nt)/(nt-1)$$

*For this to apply, care must be taken to ensure (as done in this version) that, once a curve has hit any part of a peak, this entire peak should be "flagged out", i.e., not counted should it be hit again (one year later) by the same curve. This feature, not included in earlier versions of ELEFAN 1 completely suppresses the possibility of ESP/ASP values >1, prevents "drifting" of K toward impossibly low values (see Pauly et al. 1980) an in fact contributes toward reducing the negative bias associated with many estimates of K (see Introduction).

The variance v_d of the differences d(incr) is calculated in the same way. The smaller this v_d is, the more of the empirical variance v_e is explained by the current set of growth parameter values.

The index:

$$GT = (v_e - v_d)/v_e \quad \text{(or GA for age-at-length data)}$$

is an index for the goodness of fit (similar to r^2) of the growth parameters applied to the tagging data. If the fit is perfect, then all d(incr) = 0 and $v_d = 0$, which leads to the maximum possible value GT = 1 (or GA = 1). Note that, GT or GA is automatically set to zero if $v_e - v_d < 0$.

Combined goodness of fit indices

In Table 8, computations for indices of goodness of fit are given for any possible combination of data types considered in this version of ELEFAN 1.

Table 8. Computation of goodness-of-fit index for different combinations of data type (+ = used; - = not used).

DATA TYPE			INDEX OF GOODNESS OF FIT
length-freq.	tagging	length/age	
+	-	-	ESP/ASP
+	+	-	(ESP/ASP+GT)/2
+	-	+	(ESP/ASP + GA)/2
+	+	+	(ESP/ASP + GT+ GA)/3

Optimization of the ESP/ASP ratio

In the previous sections we explained how, for a given set of growth parameter values, a single value of ESP is obtained and how the ESP/ASP ratio is calculated.

The main purpose of ELEFAN 1B is to find the growth parameters leading to the optimal ESP/ASP ratio, i.e., the best fitting growth curve. In the following, we will refer only to one growth function, the von Bertalanffy growth function modified for seasonal oscillations in growth (Pauly and Gaschütz 1979):

$$L_t = L_\infty (1 - e^{-K\{(t-t_o) + c/2\pi * \sin(2\pi * (t-t_s))\}})$$

where:

L_∞ = asymptotic length
K = growth coefficient
C = constant expressing the amplitude of growth oscillation
t_s = starting point of oscillation with respect to t = 0
t_o = origin of the growth curve
L_t = length at age t

The winter point (WP) used in the ELEFAN programs is defined as the point of slowest growth within the year and is equal to t_s + 0.5. Obviously this equation reduces to the usual von Bertalanffy function when C = 0.

*This refers to a routine suggested by Morgan (1987) and incorporated in an earlier version of the package.

The constant t_0 cannot be estimated from length-frequency data alone. The ELEFAN programs use an internal "t_0", whose value depends on the starting point of the growth curve in the length-frequency data matrix. This internal "t_0" value is not equal the t_0 value of the von Bertalanffy equation!

It is for the purpose of identifying, from among the millions of growth curves that are possible, a single "best fitting" growth that the power of a computer is actually most needed. The reason for this is that there is no continuous function which could be used to express the relationship between a given set of growth parameter values and the ESP/ASP ratio they generate. This implies that any search for an optimum combination of growth parameter values will have to be partly human-aided. In the case of ELEFAN 1B, this human input involves, as suggested by Rosenberg and Beddington (1987):

(i) identification of a (preferably narrow) range of growth parameter values between which the "true" values are expected, and

(ii) examination of the response surface, which should in the ideal case, have a single clearly identifiable area with high ESP/ASP values (in cases where L_∞ is the ordinate and K the abscissa, this area should have the shape of an elongated ellipse, suggestive of similar ESP/ASP for low values of K combined with high values of L_∞ and vice versa, see Table 10).

Actual run of ELEFAN 1B

After a data file has been loaded, the ELEFAN 1B submenu below appears on screen.

For any of the options above, ELEFAN 1B requires seeded values for (a) starting point and starting length necessary for the computation of interal "t_0" value and (b) initial estimates of the VBGF growth parameters (K, L_∞, C and WP).

```
*** ELEFAN 1B ***

RESPONSE SURFACE                <1>
NARROW SEARCH                   <2>
GROWTH CURVE COMPUTATION        <3>
QUIT TO ELEFAN MAIN MENU        <4>

* NOTE: Computation and display of correlation
  between ESP/ASP and GT (and/or GA) for
  option <3> have been deleted in this version.

                    SELECT NUMBER :
```

<1> RESPONSE SURFACE CALCULATION

This routine computes an ESP/ASP-ratio matrix for a fixed starting point. Any combinations of two of the growth parameters K, L_∞, C, WP can be held variable, while the other two are kept constant. The resulting matrix shows the response of the ESP/ASP-ratio to changes in the growth parameters and gives an impression of the reliability of the "best" growth parameter estimates (as in Brouard and Grandperrin 1984, and see Introduction). Input requirements for this option are:

i) Coordinates of starting point

ENTER SAMPLE # :
LENGTH :

ii) Upper and lower limits of the growth parameters

K : LOWER LIMIT
UPPER LIMIT

L_∞ : LOWER LIMIT
UPPER LIMIT

C : LOWER LIMIT
UPPER LIMIT

WP : LOWER LIMIT
UPPER LIMIT

In this routine, the lower limit of L_∞ is allowed to be smaller than the largest size class in the samples, but it must be greater than the starting length.

The response surface is calculated and displayed. Output on lineprinter is possible (see Table 9).

Table 9. Printout of a "Response Surface" for *Syndosmya alba* (ELEFAN 1B).

B:SYSF11R.DAT

RESPONSE SURFACE CALCULATION
K : .5 – 1.5
L_∞ : 14 – 20
C : 1.18 – 1.18
WP : .18 – .18

STARTING POINT :
SAMPLE # : 3
LENGTH : 4.41

K	RESPONSE SURFACE (table values = (ESP/ASP)*1000)									
.5	-38	-12	101	-188	-297	-265	-165	114	61	85
.61	-19	-211	-326	-156	-15	204	107	85	121	184
.72	-211	-293	34	198	135	67	219	540	564	615
.83	-202	55	171	135	158	512	601	615	667	550
.94	20	163	214	473	573	601	694	583	472	417
1.06	163	352	506	573	601	611	494	417	249	176
1.17	343	484	573	681	622	439	249	275	69	69
1.28	484	497	653	522	439	249	81	69	105	105
1.39	484	653	508	466	271	69	69	105	110	180
1.5	484	480	453	298	69	-3	105	151	180	175
L_∞	14		15.33		16.67		18		19.33	
		14.67		16		17.33		18.67		20

<2> NARROW SEARCH

Selecting this option leads the user to another submenu for a choice on how to vary the starting point. Three possible options exist:

i) Fixed starting point.
A given length in a given sample is used as starting point.

ii) Starting point variable but close to a given point.
Starting point is varied within an interval of +/- 1/2 length class. The point selected is the midpoint of an interval +/- 1/2 length class, the latter of which is divided into 10 parts of equal size.

iii) Variable starting point.

This routine, in addition to changing the values, each parameter that is kept variable also identifies the starting point giving the highest ESP/ASP ratio.

For selections i) and ii) the program requires inputs for the coordinates of starting point.

ENTER SAMPLE # :
LENGTH :

The user is then asked for search intervals for each of the growth parameters and the procedure is described below:

GROWTH COEFFICIENT K:
FIXED K <0> OR VARIABLE K <1>:
VALUE OF K?

A rather good empirical rule for first estimation of K is K = 3/lifespan. If K is to vary, a search interval must be selected. This is achieved by entering a stepsize for K, the interval has a range of K +/-3 * stepsize.

ENTER STEP SIZE OF K (FOR 3 STEPS TO BOTH SIDES)

(e.g., if K = 1.0 and STEP SIZE = 0.2, the search interval is 1.0 +/-0.6 and the following seven values of K are used for growth curve calculations: K = 0.4, 0.6, 0.8, 1.0, 1.2, 1.4, 1.6).

ASYMPTOTIC LENGTH L_∞:
FIXED L_∞ <0> OR VARIABLE L_∞ <1> :
VALUE OF L_∞?

If L_∞ is to vary, the program displays:

LOWER LIMIT OF L_∞ (upper limit of highest length class)
ENTER STEP SIZE OF L_∞ (3 STEPS TO BOTH SIDES):

A first estimation of L_∞ can be: maximum length in data set divided by 0.95. Another approach to obtain a first estimate of L_∞ is through the ELEFAN 2B program (see Introduction).

SEASONAL OSCILLATION IN GROWTH: AMPLITUDE CONSTANT C (0 <=C)
SET C = 0 IF GROWTH OSCILLATIONS ARE NOT APPARENT

FIXED C <0> OR VARIABLE C <1> :
VALUE OF C ?

If variable mode is selected:

ENTER STEP SIZE OF C (2 STEPS TO BOTH SIDES) :

If C > 0, a value for the winter point (WP), i.e., the time of slowest growth within the year, must be selected.

WINTER POINT WP (0 < = WP < 1)
FIXED WP<0> OR VARIABLE WP <1>:
VALUE OF WP ?

If the variable mode is selected:

ENTER STEP SIZE OF WP (2 STEPS TO BOTH SIDES):

then, all parameters entered are displayed and the input procedure is repeated if necessary.

Do not allow too many parameters to vary at the same time! Table 10 gives an impression of the number of calculations related to different combinations of fixed and variable parameters (with starting point *fixed*).

Table 10. Number of growth curves iterations for different growth parameter combinations (fix. = fixed, var. = variable).

Parameter	no. of steps		mode				
	fix.	var.					
K	1	7	fix.	var.	var.	var.	var.
L_∞	1	7	fix.	fix.	var.	var.	var.
C	1	5	fix.	fix.	fix.	var.	var.
WP	1	5	fix.	fix.	fix.	fix.	var.
	number of runs		1	7	49	245	1225

When working with a slow microcomputer, a rather economic strategy is to make a first run with all growth parameters fixed while varying the starting point. In the following runs the growth parameters may be varied while holding the starting point fixed.

During the search routine the following information is displayed:

Values of K, L_∞, C WP and the best ESP/ASP ratio, SAMPLE No, LENGTH

<3> GROWTH CURVE CALCULATION

This option simply computes growth curve points for the 15th of each month for a given starting point and parameter values. This allows the user to superimpose a growth curve on length-frequency data by connecting each point of the 15th of each month (Fig. 2). Output on lineprinter is possible in this option (see Table 11).

Table 11. Growth curve points on the 15th of each month for *Syndosmya alba* (ELEFAN 1B).

B:SYSF11R.DAT
RESTRUCTURED LENGTH DATA

v.BERTALANFFY GROWTH CURVE FITTED TO THE DATA

GROWTH-PARAMETERs: K = 1.22
L_∞ = 15.1
C = 1.18
WP = .18
STARTING POINT: SAMPLE 4, LENGTH 8.74

Month	1	2	3	4	5	6	7	8	9	10	11	12
								2.1	4.7	6.6	8.0	8.7
	9.1	9.1	9.0	9.0	9.1	9.7	10.4	11.3	12.0	12.6	13.0	13.2
	13.3	13.3	13.3	13.3	13.3	13.5	13.7	14.0	14.2	14.4	14.5	14.5
	14.6	14.6	14.6	14.6	14.6	14.6	14.7	14.8	14.8	14.9	14.9	14.9
	14.9	14.9	14.9	14.9	14.9							

2.6 ELEFAN 2A: Calculation of seasonal recuitment pattern and estimation of total mortality and related parameters

ELEFAN 2A is used for the calculation of (a) the seasonal recruitment pattern of the population and for the estimation of (b) the mortality (and related parameters) of the population in question by means of a "length-converted catch curve".

Seasonal recruitment patterns

A recruitment pattern is a graph whose peaks and troughs reflect the seasonality of recruitment to the stock in question. If a set of length-frequency data and a corresponding set of growth parameter values are available, the recruitment pattern can easily be computed by projecting each length-frequency sample backward onto the time axis. In other words, if we calculate the time at which length was zero for each length class of every sample and sum up the abundance of each point of our data matrix (length, sampling time) in the corresponding time interval (here, 12 invervals = 1 year), the result will be a seasonal recruitment pattern.

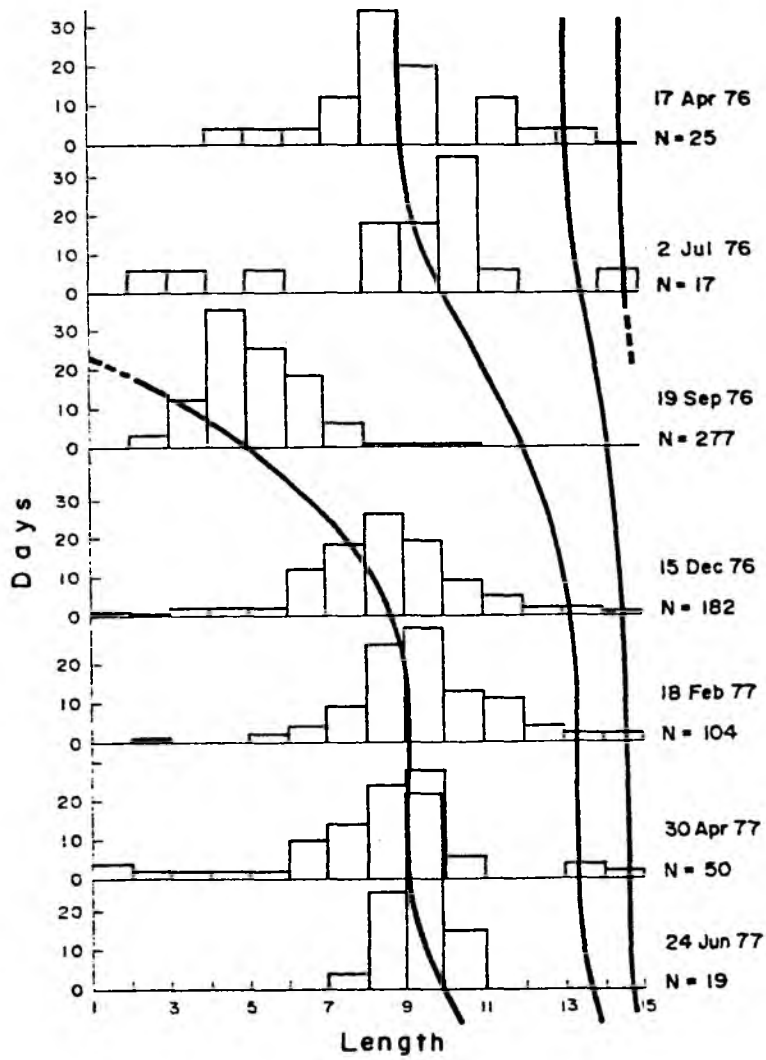


Fig. 2. Length-frequency data of *Syndosmya alba* with superimposed growth curve fitted using ELEFAN 1 B.

ELEFAN 2A uses a more complex computation procedure correcting for the fact that growth is not linear.

i) Each length class, in each sample, is divided into 10 intervals.

ii) The value added to the recruitment pattern memory is $N_1/10$ divided by the time required to grow through the length interval in question.

iii) The lowest monthly recruitment value is subtracted from all 12 values resulting in at least one zero value corresponding to the month of lowest recruitment. The resulting distribution is converted into relative frequency.

Because the value of t_0 of the von Bertalanffy function is usually not known (which implies that the absolute age of the animals is unknown), the exact position of the recruitment pattern within the year will usually not be known either. However, examination of the length-frequency samples may suggest the time of highest recruitment within the year, especially when small sizes are represented in the samples.

Mortality and the concept of a "length-converted catch curve"

For ecologists, the estimation of catch curves is the most interesting part of the ELEFAN package because a "length-converted catch curve" is a way to estimate the annual P/B-ratio of the investigated population. Allen (1971) showed that the total mortality Z of a steady-state population is equal to the P/B-ratio, if mortality can be expressed by a single negative exponential function and if the individual growth can be described by a von Bertalanffy function.

The "length-converted" catch curve is a simple way to estimate the mortality of a population if the growth parameters are known and if the assumption of stable-age distribution implied in catch curve-based methods is reasonable (see below).

Theory of catch curves

Catch curves are usually constructed for the investigation of the mortality within natural fish populations (see Ricker 1975). Essentially they consist of a plot of the natural logarithm of the abundance of various age classes N(t) against their corresponding age t, as shown in Fig. 4.

The ascending left part of the plot is due to the decreasing catch efficiency of the gear with decreasing size of fish. The descending right part of the plot can be ascribed to mortality within the population. If the mortality of the population follows a single negative exponential model,

$$N_t = N_0 * e^{-Z*T}$$

then a catch curve will show a generally straight descending right arm, which can be described by a linear equation, i.e., the logarithmic form of the equation above

$$\ln(N_t) = a + b * t$$

If the individual age of the animals is not known, a "length-converted" catch curve can be used in the same way as described above to determine the total mortality Z (Pauly 1982, 1983a, 1983b, Gulland 1983, p. 104-105; Pauly 1984a, 1984b, 1984c, chapter 5).

The "length-converted" catch curve as used in ELEFAN 2A consists of a plot of $\ln(N_1/\Delta t)$ against relative age t_1, where N_1 is the number of animals in the i^{th} length class and Δt is the time required by an average animal to grow through this length class (all of which can be easily computed if the growth parameter values are known).

The regression function for the estimation of Z is then

$$\ln(N_1/\Delta t) = a + b * t \quad \text{and} \quad Z = -b$$

The following assumptions are involved in the estimation of Z from a "length-convered" catch curve:

(i) Z is constant over all age/size classes included in the plot.
(ii) Recruitment fluctuations (with respect to all age classes considered in the plot) have been small and of random character.
(iii) The gear used has a selection curve such that only the smaller animals are selected against.
(iv) The sample used represents the average population structure over the time considered.

Calculations involved in the estimation of Z

Three major steps are involved in the estimation of mortality (Z):

(a) Pooling of individual samples

This is particularly needed in short-lived benthic animals, because their population structure is affected by seasonal recruitment pulses. To prevent sampling errors from unduly affecting the total sample, several options of weighting the periodic samples prior to pooling in the large sample are offered.

In general, samples are not adjusted if the data represent a single cohort. The conversion to % length frequency has the effect of giving the same weight to each sample. In some cases, e.g., if the sampling area is not equal for all samples and sampling is affected by large random deviations, it may be appropriate to, additionally, weight the samples by the square-root of their size. Two other (optional) weighting procedures may also be considered:

i) Weighting with respect to distance in time (time elapsed between samples, as suggested by J.L. Munro, pers. comm.).

If the distances in time between the single samples within the year are not equal, a higher weight may be given to more isolated samples (J. L. Munro, pers. comm.). For each sample this weight corresponds to the distance dt (as fraction of year) to the nearest sample. Each frequency of the sample is weighted by

$$F_1 = F_i * (1 + 2*\Delta t)$$

ii) Weighting with respect to seasonal oscillations in growth

If the growth oscillation constant C of the seasonally oscillating von Bertalanffy equation exceeds 1, a certain period of stagnation in growth and/or negative growth occurs around the winter point WP. This affects the estimation of Z through the catch curve. If more than one sample is included in the period of stagnation, these samples can be pooled separately into one "winter-sample", which is representative for the period of growth stagnation.

(b) Construction of the catch curve

All steps included in the computation of the "length-converted" catch curve are demonstrated in Table 11 using the pooled samples from Table 1. The relative age at the lower limit, the upper limit and their mean (t_{low}, t_{high} and t_{mean}, respectively) are given by

$$t = \ln(1 - (L_t/L_\infty))/K$$

The time required to growth through a length class, Δt is

$$\Delta t = t_{high} - t_{low}$$

The catch curve is constructed using $\ln(\%N/\Delta t)$ and t_{mean}.

Table 12. Construction of "length-converted" catch curve for *Syndosmya alba*, using K = 1.22, L_∞ = 15.1.

	Class limits lower	upper	mid-length	N	t_{low}	t_{high}	Δt	$N/\Delta t$	$\%(N/\Delta t)$	$\ln(\%N/\Delta t)$	t' mean years
1	1.0	2.0	1.5	4	.056	.116	.060	66.338	1.037	0.036	0.086
2	2.0	3.0	2.5	13	.116	.181	.065	199.731	3.121	1.138	0.148
3	3.0	4.0	3.5	39	.181	.252	.071	551.586	8.619	2.154	0.216
4	4.0	5.0	4.5	101	.252	.330	.077	1305.161	20.394	3.015	0.290
5	5.0	6.0	5.5	77	.330	.415	.085	901.008	14.079	2.645	0.371
6	6.0	7.0	6.5	81	.415	.510	.095	848.893	13.265	2.585	0.461
7	7.0	8.0	7.5	69	.510	.619	.108	638.845	9.982	2.301	0.563
8	8.0	9.0	8.5	104	.619	.743	.124	835.803	13.060	2.570	0.678
9	9.0	10.0	9.5	97	.743	.890	.147	660.939	10.328	2.335	0.813
10	10.0	11.0	10.5	43	.890	1.069	.179	240.363	3.756	1.323	0.974
11	11.0	12.0	11.5	24	1.069	1.298	.229	104.727	1.636	0.493	1.175
12	12.0	13.0	12.5	9	1.298	1.617	.319	28.193	0.441	-0.820	1.442
13	13.0	14.0	13.5	8	1.617	2.147	.530	15.094	0.236	-1.445	1.840
14	14.0	15.0	14.5	6	2.147	4.113	1.965	3.053	0.048	-3.043	2.644

(c) Estimation of Z

Using the catch curve plot displayed and the listing of catch curve points (see Table 13), it can then be decided whether the single negative exponential mortality model adequately describes the mortality of the population in question. If this appears to be true, the points to be included in the computation of Z are selected. This is the most sensitive part of the whole procedure. Usually the first point selected (P_1 in Fig. 3) should be the point immediately to the right of the highest point. In small bivalve molluscs, however, the selection curve of the sieve used is often very steep, so the highest point can often be included. At the right end of the plot, points should not be included which correspond to lengths greater than 95% of L_∞ and/or based on a few (<5) animals only. A first estimate of Z, Z' is calculated by linear regression over the selected points. Then, an iteration procedure (due to P. Sparre, pers. comm.) corrects this Z' for the nonlinearity of the growth model and for the fact that some mortality occurs within each length class:

$$\ln(N_1/(1-e^{-Z_j * t_i})) = a - Z_{j+1} * t_i$$

where i is the length class number, t_i is the relative age at the *lower* limit of length class i, Z_j and Z_{j+1} are initial and improved estimates of Z, respectively (see also Pauly 1984c).

An additional procedure for this routine is,

(d) Selection curve and mean length at first capture

If the natural mortality (M) of the population in question is known, the selection curve of the gear can be inferred from the shape of the ascending left part of the catch curve (see Pauly 1980 for an empirical equation to estimate M in fish populations from L_∞, K and mean environmental temperature).

The selection curve is computed by setting up a table of probabilities of capture for the length classes not fully selected by the gear. Table 14 shows a table of probabilities of capture, based on the results given in Table 13. Details are as follows:

i) delta T (Δt) is the time between two corresponding midlengths L_i and L_{i+1}.

Table 13. Printout of catch curve points (ln (%N/Δt) on relative age) and midlengths and frequencies of *Sydosmya alba* data (ELEFAN 2A).

B:SYSF11.DAT
Syndosmya alba / SF 0.4.1976 — 06.1977 / 1mm classes

WEIGHTING MODE No 1
WEIGHTING BY TIME: NO
WEIGHTING (C, WP): NO
GROWTH PARAMETERS: L_{∞} = 15, K = 1, C = 0, WP = 0

No.	Midlength	N	LN(%N/delta T)	Relative Age
1	1.5	4	4.188585E-02	.1053606
2	2.5	13	1.143503	.1823216
3	3.5	39	2.158637	.2657032
4	4.5	101	3.019097	.356675
5	5.5	77	2.647533	.4567585
6	6.5	81	2.586718	.5679841
7	7.5	69	2.300886	.6931473
8	8.5	104	2.567573	.836248
9	9.5	97	2.330054	1.003302
10	10.5	43	1.314499	1.203973
11	11.5	24	.4773121	1.455287
12	12.5	9	-.8466956	1.791759
13	13.5	8	-1.500687	2.302582

Table 14. Printout of total mortality and probabilities of capture for *Syndosmya alba* (ELEFAN 2A).

B:SYSF11.DAT
Syndosmya alba / SF 04.1976 — 06.1977 / 1mm classes

PROBABILITIES OF CAPTURE, BY LENGTH
WEIGHTING MODE No. 1, POINTS INCLUDED: 9 — 12
WEIGHTING (TIME): NO
WEIGHTING (C, WP): NO
GROWTH-PARAMETERS: L_{∞} = 15, K = 1, C = 0, WP = 0

TOTAL MORTALITY Z = 3.968973
NATURAL MORTALITY M = 3.968973
(REGRESSION LINE: Y = ln (%N/(1 — exp (—Z*delta t)) vs X = Relative age
a = 8.786342, b = —3.968973, corr. coeff. r = —.9968694)

Midlength	N caught	delta T	Mortality 1	Mortality 2	N available	P
1.50	4.000	0.14384	3.9690	3.9690	3424.176	0.0012
2.50	13.000	0.22401	3.9690	3.9690	2522.889	0.0052
3.50	39.000	0.31119	3.9690	3.9690	1812.062	0.0215
4.50	101.000	0.40672	3.9690	3.9690	1262.888	0.8000
5.50	77.000	0.51237	3.9690	3.9690	848.888	0.0907
6.50	81.000	0.63057	3.9690	3.9690	545.922	0.1484
7.50	69.000	0.76470	3.9690	3.9690	332.190	0.2077
8.50	104.000	0.91978	3.9690	3.9690	188.245	0.5525
9.50	97.000	1.10364	3.9690		97.000	1.0000

Mean length at first capture = 7.8928.

ii) Mortality 1 is the mortality *within* a length class. It is calculated by interpolation between M (mortality in the highest length class not caught at all) and Z (i.e., the mortality from point P_1 on). The step size for the interpolation is estimated from (Z-M)/(n+1) where n is the number of classes for which mortality must be interpolated (here, n=3).

iii) Mortality 2 is the mortality occurring *between* adjacent length classes. It is calculated as the mean between the Mortality 1 values of adjacent length classes. The number of animals available in each length class (Nav), is calculated by

$$Nav_i = Nav_{i+1} * e^{Mortality\ 2} * \Delta t$$

where Nav_1 is the number available in length class i and Nav_{i+1} the number available in the next higher length class. Therefore this calculation has to be started with the length class next to the class with Mortality 1 = Z.

iv) N caught is the number of animals that were actually caught.

v) P, the probability of capture for each length class i is calculated using,

$$P_i = Ncaught_i/Nav_i$$

The mean length at first capture L_c is the length corresponding to a cumulative probability of capture of 0.5 (=50%). In marine benthic invertebrates the natural mortality M usually equals the total mortality Z because no fishery impacts on the population. In such cases, the calculation of Mortality 1 and Mortality 2 is superfluous.

Actual run of ELEFAN 2A

After a length-frequency data file is loaded and the growth parameter values are entered, the following menu appears:

```
*** ELEFAN 2A ***

RECRUITMENT PATTERN                <1>
TOTAL MORTALITY                    <2>
QUIT TO ELEFAN MENU                <3>
              SELECT NUMBER :
```

The pooling and weighting procedures follows for selections <1> and <2):

```
*** ELEFAN 2A ***
OPTIONAL INPUT : WEIGHTING/RESTRUCTURING OF SAMPLES

NO WEIGHTING/RESTRUCTURING:                <1>
WEIGHTING BY SQUARE ROOT OF SAMPLE SIZE:   <2>
CONVERSION TO % LENGTH-FREQUENCY:          <3>
QUIT TO ELEFAN 2A MENU:                    <4>
                        SELECT NUMBER :

WEIGHTING WITH RESPECT TO DISTANCE IN TIME?   (Y/N):
```

Each sample is displayed. Original and weighted values are presented. The user is allowed to exclude certain samples from further processing. If the amplitude constant C of growth oscillations exceeds 1, weighting with respect to growth stagnation is possible.

WEIGHTING WITH RESPECT TO C AND WP? (Y/N):

After this procedure the "status" of each sample is displayed:

STATUS OF SAMPLES
0 = EXCLUDED, 1 = INCLUDED, 2 = WEIGHTED WITH RESPECT TO C AND WP
No. STATUS

and the samples are pooled.

The program will then go into different subroutines, depending on the option selected through the ELEFAN 2A menu.

<1> RECRUITMENT PATTERN

To run this routine, estimates of the growth parameters are inputed from the keyboard, in the same manner as in the previous program, after which the calculation of recruitment pattern begins. The computations take a little, after the display appears on screen, it may be printed out on a lineprinter as shown in Fig. 3 or run may be done following a change in weighting mode and/or the input of different growth parameters.

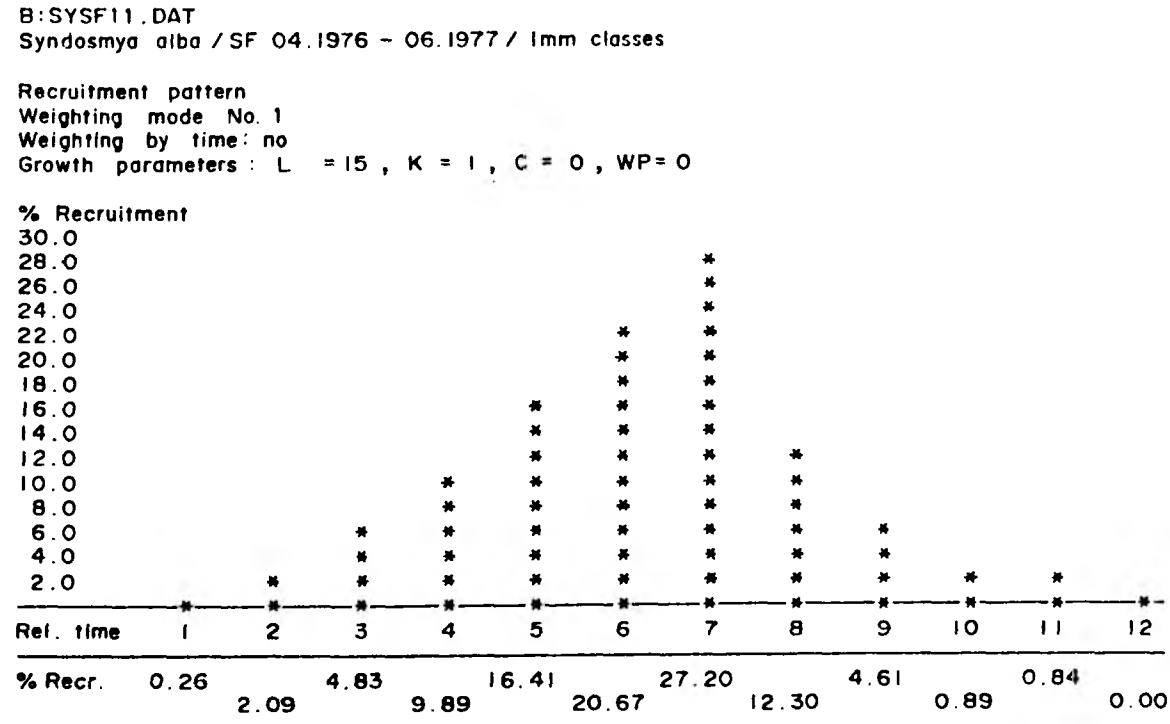


Fig. 3. Outputs on recruitment pattern for *Syndosmya alba* (ELEFAN 2A).

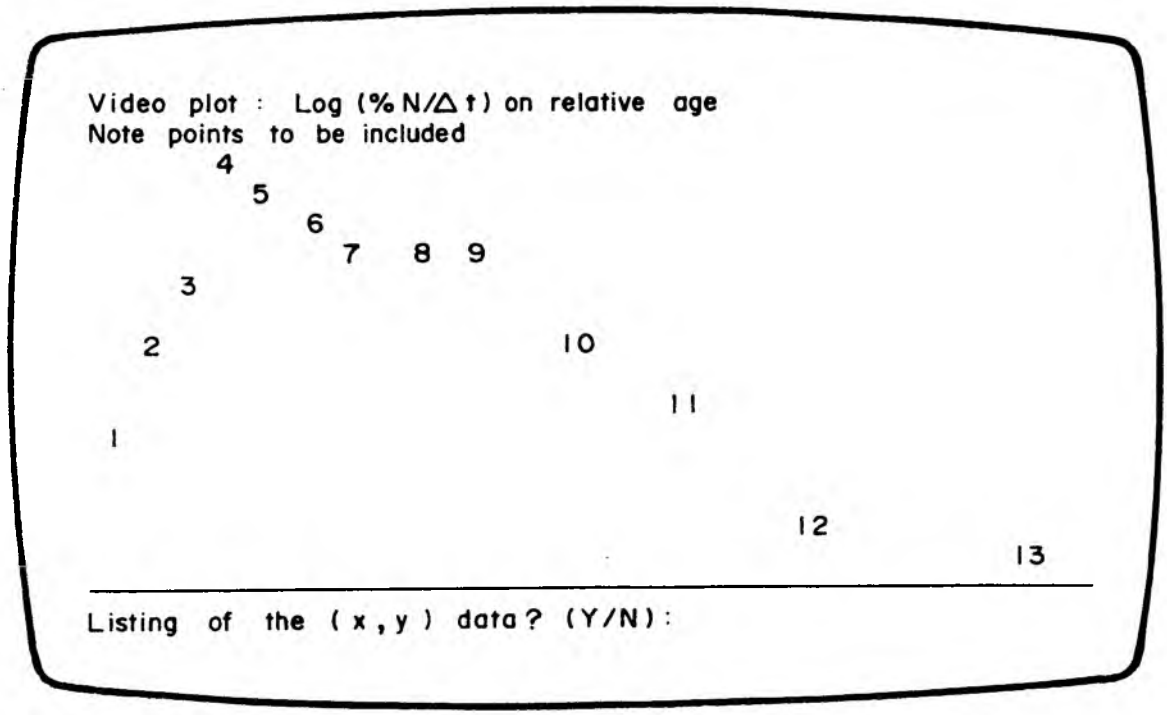
<2> TOTAL MORTALITY

Before proceeding to the estimation of total mortality, a check for zero frequency values in any length class of the pooled sample is made. Further processing is stopped when zero frequencies are encountered because log(0) is undefined. The message appears:

ZERO FREQU. VALUE(S) INCLUDED IN DISTRIBUTION!
FURTHER CALCULATION IMPOSSIBLE!

When this happens, a value of 1 can be inserted in the original length-frequency distribution of one single sample, or the data can be regrouped into larger length classes (both options are performed using ELEFAN 0). ELEFAN 2A then returns to the menu

If no zero frequency occurred, a videoplot of the catch curve is displayed:



Each point is represented by the number of the corresponding length class. Then, the question is asked:

LISTING OF THE (x,y) DATA? (Y/N):

If Y is entered, the data are listed. Output on lineprinter is possible.

Then, the points for the estimation of Z are selected.

CONSTRUCTION OF THE CATCH CURVE
ENTER FIRST POINT (No) TO BE INCLUDED:
ENTER LAST POINT (No) TO BE INCLUDED:

Estimates of Z', Z, regression parameters are computed and the results displayed on screen.

For the construction of a table of probabilities of capture, a value of the natural mortality M must be entered.* The selection curve is computed and displayed. Output on lineprinter is possible as shown in TabLE 13.

Further calculations are optional:

NEW CALCULATION OF Z WITH OTHER POINTS? (Y/N):
NEW CAL. WITH DIFFERENT WEIGHTING MODE? (Y/N):

2.6 ELEFAN 2B

Program ELEFAN 2B is used to obtain a first estimation of L_∞ and Z/K without any information about growth itself being available. The method and equations implemented here are due to Wetherall (1986) and Wetherall et al. (1987), to whom reference should be made in papers based on this routine (see Introduction).

The method applies only if the single negative exponential mortality model fits the data, and if a stable age distribution can be assumed. The program first displays a curve (Fig. 4) with N (length class) on the Y-axis and length on the X-axis. If this plot has a smoothly, monotonically descending left arm, the estimation of L_∞ will be reasonable, otherwise not.

The user then selects one point (P_1) of the curve, at the left of which the data must be ignored because of selection effects.

Now X/Y data points are calculated, from i = P_i to the last point, where

X_i = lower limit of length class
Y_i = mean length over all classes above and including i
N_i = cumulative frequency up to class i.

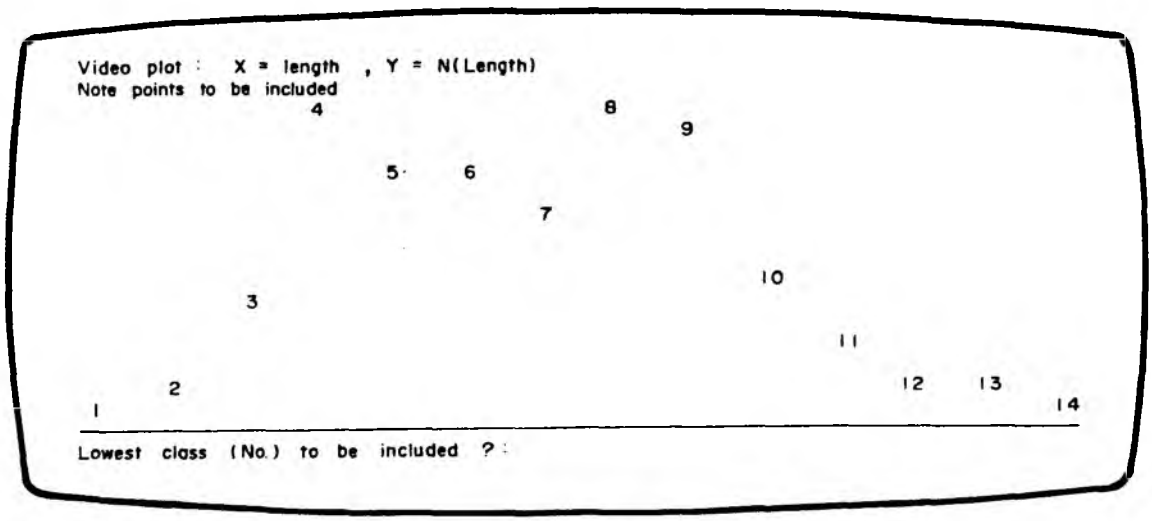


Fig.4 . Plot of length class frequency on midlength of *Syndosmya alba* (ELEFAN 2B).

*Pauly (1984a) has shown that the estimates of mean length at first capture L_c obtained through this routine are relatively independent of the value of M entered; thus, entering Z=M will provide reasonable estimates of L_c. The curve discussed here is, rigorously speaking, not a "selection" but a "resultant" curve, i.e., the product of a gear selection curve with a recruitment curve (see Gulland 1983, p. 127). Therefore, values of L_c estimated by the procedure outlined here will tend to be higher than estimates of L_c obtained from selection experiments. This effect can be counteracted by using here, for the estimation of L_c only, those length-frequency samples which include small animals, i.e., sample collected during the recruitment season (Y. Mokhtar, pers. comm.).

In the original form of this method, L_∞ and Z/K are estimated from a regression line to the x/y data, where

$$Y_i * N_i = a + b * X_i * N_i \text{ (regression equation)}$$

$$L_\infty = a / (1-b)$$

$$Z/K = b / (1-b).$$

However, the method implemented here is the form suggested by Pauly (1986), where

$$(Y_i - X_i)*N_i = a + b*X_i*N_i$$

$$L_\infty = a/-b$$

$$Z/K = (1+b)/-b$$

Actual Run of ELEFAN 2B

The loading of data file, selection of samples, weighting and pooling of samples are exactly as described in ELEFAN 2A. After all the relevant queries have been answered, the length-frequency plot is shown on screen (Fig. 4) and first point (P_i) to use in the regression equation is asked for.

Following entry of P_i, estimates of L_∞ and Z/K and a regression plot are displayed on the screen and output to line printer is possible (Table 14). Finally, the user may rerun the program with a different starting point or return to the ELEFAN main menu.

Table 15. Printout of *Syndosmya alba* data used for estimation L_∞ and Z/K, estimates of L_∞ and Z/K and regression plot (ELEFAN 2B).

L(mean)-L'	L'(x-axis)	N(cumulative)
6.314815	1	675
5.349478	2	671
4.445289	3	658
3.693861	4	619
3.316603	5	518
2.80839	6	441
2.327778	7	360
1.761169	8	291
1.462566	9	187
1.5	10	90
1.414893	11	47
1.369565	12	23
.9285717	13	14
.5	14	6

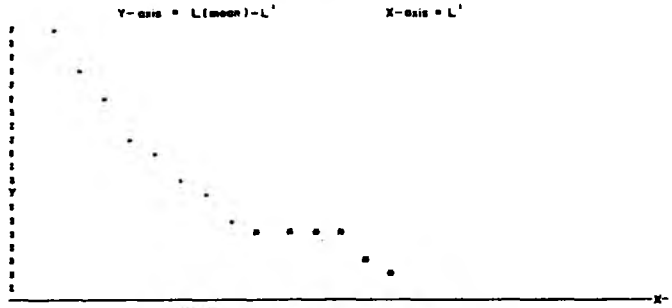
Estimation of Asymptotic length and Z/K

Regression equation : X = lower limit of smallest length class
Y = mean length over all classes
Lowest class included : Lengthclass No. 9

Y = 2.389709 + (-9.734258E-02 * X) ; r = -0.7406525 , r^2 = 0.5485661

Estimate of L_∞ : 24.54943

Estimate of Z/K: 9.272996



(To draw regression line simply link Y and X intercepts.
Imprecise location of the line is due to text mode plotting.
Please use regression equation to draw line when accurate graphs are needed.)

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